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The sawflies (Hymenoptera, Tenthredinidae) of Greenland

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Abstract

The sawfly fauna of Greenland is reviewed, based on specimens collected in 2025 and a re-examination of material in museum collections. *Ametastegia pallipes* (Spinola, 1808) and *Euura vaga* (Fabricius, 1781) are recorded from Greenland for the first time. *Pristiphora laricis* (Hartig, 1837) is confirmed to be well established in a restricted area of South Greenland. *Euura obscuripes* (Holmgren, 1883) is the valid name for the nominal taxa described from Greenland as *Nematus borealis* Marlatt, 1892 (new synonym) and *Amauronematus groenlandicus* Malaise, 1933 (new synonym). Greenlandic specimens of *Euura cornuta* (Lindqvist, 1962) have formerly been misidentified as *Amauronematus viduatus* (Zetterstedt, 1838) or *A. nitidipleuris* Malaise, 1931. Now including a total of only nine recorded species, the sawfly fauna is extremely species-poor, thus fitting the general pattern exhibited by most groups of insects in Greenland. Genetic sequencing and existing distribution data indicate that most species are likely to have reached Greenland from the West Palaearctic. The possibility that some of them may have been accidentally introduced by humans is discussed.

Key Words

Allantinae, colonisation, DNA barcoding, host plants, Nematinae, new records, new synonyms, Symphyta

Introduction

The insect fauna of Greenland has long fascinated entomologists, particularly Europeans (Henriksen 1939). Rather recently, the accumulated knowledge was compiled in a monograph by Böcher et al. (2015).

A benchmark inventory of the sawfly fauna of Greenland was provided by Vilhelmsen (2015), who considered six species of Tenthredinidae to be reliably recorded: five species that are currently placed in the genus *Euura* (Nematinae), and an unidentified species of *Ametastegia* (Allantinae). Goulet and Bennett (2021) listed seven sawfly species from Greenland, all belonging to *Euura*. The difference between these publications in the number of treated species arises from the inclusion by Goulet and Bennett (2021) of *Euura borealis* (Marlatt, 1892) and *E. parvilabris* (Thomson, 1863) and their omission of *Ametastegia* sp.

With the main aim of collecting sawflies, the authors visited southern Greenland from mid-June to early July 2025. Here, some new faunistic data are presented, and an attempt to shed light on the origin of the Greenlandic sawfly fauna is made by comparing gene sequences obtained from the fresh material with sequences of the same species from other parts of the world.

Material and methods

Böcher et al. (2015: fig. 1 [map], p. 22) is followed in the subdivision of Greenland into zoogeographic regions.

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Fieldwork was conducted in and near Narsarsuaq, South Greenland (S), from 13–24 June 2025, and around Nuuk and Kapisillit, southern South-West Greenland (sSW), from 25 June–3 July 2025. Most specimens were obtained by sweeping vegetation using entomological nets.

Selected genera of plants, known to be hosts of sawflies in other parts of the world, were searched visually for larvae and feeding traces, such as galls and leaf mines.

Most specimens were killed by freezing and pinned shortly thereafter. For genetic analysis, legs of some specimens were detached and placed in 96% ethanol, or whole specimens were conserved in ethanol.

Coordinates of the localities are for the centre of a field of collecting activity with a maximum radius of 3.5 km:

Narsarsuaq; 61.167, –45.417
Qassiarsuk [Brattahlíð]; 61.154, –45.521
Nuuk; 64.180, –51.670
Kapisillit; 64.417, –50.271

Abbreviations for collections in which examined specimens are deposited:

ANSP Academy of Natural Sciences of Drexel University, Philadelphia, USA
NHMD Natural History Museum Denmark, University of Copenhagen, Copenhagen, Denmark
OLC private collection of O. Lønnve, Oslo, Norway
SDEI Senckenberg Deutsches Entomologisches Institut, Müncheberg, Germany
SYKE Finnish Environment Institute, Finland
TUZ Natural History Museum, University of Tartu, Tartu, Estonia
ZMUN Zoological Museum, University of Oslo, Oslo, Norway

Fragments of COI and up to seven nuclear genes were sequenced for this study using an Oxford Nanopore MinION. The primers used to amplify COI were SymF5v2, SymF3v2, and A2590 (see Prous et al. 2025). The nuclear genes were PGD (PGD326F, PGD_hym_intRb), TPI (TPI35F, TPI706Rv2), EF1a F2 (EF1a167F, EF1a1213R, EF1a1213Ra), NaK (NaK_263Fv2, NaK_1918Rv2), POL2 (POL2_797F, POL2_2569R), HSP90 h1 (HSP90_59F, HSP90_1843Rv2), and TRRAP (TRRAP_833F, TRRAP_2620R) (Prous et al. 2025). An Oxford Nanopore Native Barcoding Kit 96 V14 (SQKNBD114.96) was used to multiplex PCR products, and they were sequenced on an R10.4.1 flow cell. The raw sequencing signals (pod5 files) were basecalled with Dorado 1.0.1 in super-accuracy mode, using the emit-moves option to enable more accurate consensus sequence polishing. To obtain accurate variant sequences, the base-called sequence data were processed using the modified workflow described in Prous et al. (2025). The main differences were the identification of different amplicons (genes) based on primer sequences using cutadapt 3.5 or 4.9; variant detection and read phasing using freebayes and devider (Shaw et al. 2025); and polishing of variant consensus sequences with Dorado polish. The newly obtained DNA sequences have been submitted to NCBI GenBank (accessions PX854216–PX854231, PX875218–PX875325).

The *p*-distances (proportion of nucleotide differences) were calculated in R using the package ape (Paradis and Schliep 2019) or were taken from BOLD identification engine (https://id.boldsystems.org/) results. Neighbour-joining distance trees were built with ape using the TN93 substitution model.

Results

In 2025, a total of six species were collected, all represented by adults, and three of these were also represented by larvae: larvae of two were found in the field, and one was obtained by *ex ovo* rearing. The larvae observed in the field were a few *Euura excisa*, following visual inspection of its host plant, and a single individual of *Euura vaga*, swept from low vegetation. Despite the partly fine weather experienced and the large number of man-hours spent sweeping, it seems significant that only a single sawfly larva was obtained by that method. It is therefore unlikely that a significant number of early-season sawfly species were overlooked. On the other hand, one or two species that emerge later in the season were possibly missed. Most adult sawflies were swept "unseen" from various plants, although individuals of the abundant *Pristiphora laricis* were seen several times, active or resting on their host and other woody plants. In the following commentaries on the Greenland sawfly fauna, notes are also included on species represented in museum material investigated by MP.

Ametastegia pallipes (Spinola, 1808)

Material examined. Greenland. Narsarsuaq • 1♀ (SDEI; DEI-GISHym81441), 20 June 2025, Liston leg. • 1♀ (TUZ; TUZ399063), 1 *ex ovo* larva from preceding female (TUZ; TUZ399075), 23 June 2025, Prous leg. Qassiarsuk • 4♀♀ (SDEI), 21 June 2025, Liston leg. • 1♀ (TUZ; TUZ399056), 21 June 2025, Prous leg. • 1♀ (TUZ; TUZ109608), 21 June 2025, Liston leg. • 5♀♀ (OLC), 21 June 2025, Lønnve leg.

Habitus and variability (Fig. 1). No significant differences observed. Length 6–7 mm. The legs of all specimens are very dark: metafemur nearly entirely black, and only basal half of metatibia white.

Habitats. The Narsarsuaq specimens were swept in an area between houses, where some patches of *Viola tricolor* L. occur. This *Viola* species is not indigenous to Greenland (Rune 2011). Most of the Qassiarsuk specimens

Figure 1. *Ametastegia pallipes* female (TUZ399063), body length ca. 6.5 mm (top), and a late feeding instar larva, length 15 mm (bottom), reared from it. Photos: M. Prous.

were swept near a stream where one or more native *Viola* species grow, but not *V. tricolor*, and the other specimens were from drier pasture and meadows on slopes where flowering *Viola*, probably *V. canina* L., was noted.

Host plants and biology. In Europe, several species of *Viola* have been recorded as hosts (Chawner and Peacock 1923; Lacourt 2001). One female from Narsarsuaq was induced by MP to lay eggs in *Viola tricolor*, of which two hatched, but only one larva (Fig. 1) was reared to the prepupal stage and then stored in alcohol (the other was accidentally lost). At least three annual generations have been observed in England (Chawner and Peacock 1923). *Ametastegia pallipes* is thought to be entirely parthenogenetic, with no male specimens known.

Distribution. Occurs widely in the Holarctic (Sundukov 2017; Goulet and Bennett 2021; Smith 1979), including Europe from Sicily northwards to the Arctic areas of Fennoscandia (own observations). Also recorded in Iceland (Ólafsson 1991).

Remarks. This is probably the sawfly species recorded by Vilhelmsen (2015) as *Ametastegia* sp.: "Only known from a few larvae collected in Upernaviarsuk and Narsarsuaq".

Genetics. The COI of the single sequenced specimen (TUZ399056) is one nucleotide different (0.15%) from the main widespread variant (several countries in Europe and Canada) of *Ametastegia pallipes*.

Cladius grandis (Serville, 1823)

Notes. Vilhelmsen (2015) excluded *Cladius grandis* (Serville, 1823) from the Greenlandic fauna. It was listed as occurring in Greenland by Henriksen (1939), with the only data "W. G.: [69°15']". [W. G. standing for West Greenland]. Henriksen and Lundbeck (1917) gave additional information on the single putative record of *Cladius grandis* from Greenland, under the name *Trichiocampus viminalis* (Fallén, 1808) [translated from Danish]:

"West Greenland: Of this new species for the Greenlandic fauna a female has been taken at Godhavn on Disko (Zool. Mus.). Not known from East Greenland. Geogr. Distribution: Northern and Central Europe. The larva lives on poplar, but may also occur on willow; this last is certainly the case in Greenland."

The specimen is no longer to be found in NHMD, where it was originally housed. We agree with Vilhelmsen's decision to exclude the species from the list of Greenland insects. Henriksen and Lundbeck (1917) were wrong in stating that *C. grandis* uses *Salix* as a host: its larva feeds only on *Populus* spp. There is no evidence for the use of *Salix* as a host, and occasional such statements in the literature probably arose through misidentifications of the very similar larvae of *C. aeneus* Zaddach, 1859. There is no native *Populus* species in Greenland, although some species have been planted, for example, at Narsarsuaq (but probably after ca. 1941). If the claimed Greenlandic *C. grandis* specimen was correctly identified, then the record must relate to the chance introduction of a single individual to an area where it could not become established.

Euura amentorum (Förster, 1854)

Material examined. Greenland. Nuuk • 1♀ (OLC; DEI-GISHym40555), 26 June 2025, Lønnve & Olsen leg. • 3♀♀ (OLC; including DEI-GISHym40556, DEI-GISHym40559), 3 July 2025, Lønnve & Olsen leg.

Habitus and variability (Fig. 2). Length 3.5–4.5 mm. Three specimens have pale tegula, distinctly pale rear edge of pronotum, and distinctly pale lower part of face; one specimen is darker, with black tegula, almost black pronotum, and darker lower part of face.

Host plants and biology. Larvae of all species of the *Euura amentorum* species group feed within the female catkins of *Salix* species, into which the females oviposit (Liston et al. 2023). The range of *Salix* species fed on by *E. amentorum* is very wide. *Salix* species present where adults were collected were *S. arctophila* Cockerell ex A. Heller, *S. glauca* L., and *S. herbacea* L., and some plants of all these were flowering. At least three of the specimens were swept from *S. glauca*, a host recorded for *E. amentorum* both in Canada (Humble 2006) and in northern Europe (Liston et al. 2023).

Figure 2. *Euura amentorum* female (DEI-GISHym40559), body length 4.0 mm. Photo: Stefan Olberg.

Distribution. Occurs widely in the Holarctic, including Iceland. Confirmed males have been found (only) in Europe but are very rare (Liston et al. 2023). Benson (1962) mentioned one male (North Greenland, 82°N, 31°W, 24.VI.1949) and two females (East Greenland ca. 76°46'N, VII.1908; West Greenland, Jakobshavn, ca. 69°N, 28.VI.1951), but the male may represent *Euura cornuta* (see below), which also has a penis valve with a long spine.

Genetics. The COI of two sequenced specimens (DEI-GISHym40555, 40559) is identical to many *Euura amentorum* specimens from mainland Europe (Finland, Norway, and France) and a specimen from Iceland. The COI sequences of North American (Canada and USA) specimens are 1.2–2.1% different from the specimens from Greenland. Sequenced nuclear genes of the Greenlandic specimens are also identical to each other and closest to specimens from Finland and Iceland (minimum difference of 0.1%). A specimen from the USA is 0.5% different.

Euura cornuta (Lindqvist, 1962)

Material examined. Greenland. South-East Greenland, Skjoldungen "Bygden" • 1♀ (NHMD), 19–27 July 1992, S. Andersen leg. Northeast Greenland, Zackenberg Research Station (74.467, –20.567) • 1♀ (SYKE; grhym-00070), 11 June 2010, T. Roslin leg.

This is the species called *Amauronematus viduatus* by Henriksen (1939) and *A. nitidipleuris* by Vilhelmsen (2015). Two examined females (one in Fig. 3) fit well morphologically with *E. cornuta* (black pronotum, tegula, and cerci; partly pale clypeus and malar space), but not the other known European *Euura viduata* group species.

Figure 3. *Euura cornuta* female (grhym-00070), body length 6.5 mm. Photos: Marko Mutanen.

Genetics. The COI of two specimens from Northeast Greenland (Zackenberg Research Station; grhym-00070 and ZA2011-523 in BOLD) are identical to each other and 2.4–2.5% different from European *E. cornuta*. Based on COI, *E. cornuta* is the most distinct within the *Euura viduata* group (about 7% different from the other species). However, the closest sequences to the Greenland specimens (minimum divergence of 0.15%) are unidentified *Euura viduata* group specimens from Canada (including Ellesmere Island) that may include species other than *E. cornuta* (a female BIOUG16993-E11 from Yukon in BOLD has an extensively pale pronotum and tegula).

Euura excisa (Thomson, 1863)

Material examined. Greenland. Narsarsuaq • 2♀♀ (TUZ; TUZ399053, TUZ109613), 20 June 2025, Prous leg. • 4♀♀ (TUZ; TUZ109614–7), 22 June 2025, Prous leg. • 1♀ (SDEI), 22 June 2025, Prous leg. • 1♀ (OLC), 22 June 2025, Prous leg. Nuuk • 2♀♀ (TUZ; TUZ399064, TUZ109618), 26 June 2025, Prous leg. • 7♀♀ (TUZ; TUZ109712–7, TUZ399099), 3 July 2025, Prous leg. • 17♀♀ (OLC; including DEI-GISHym40557, DEI-GISHym40558), 3 July 2025, Lønnve & Olsen leg. • 19♀♀ (SDEI), 3 July 2025, Liston leg. Kapisillit • 1 larva (TUZ; TUZ399073), 28 June 2025, Prous leg. • 15♀♀ (TUZ; TUZ109619–29, TUZ399068,

TUZ399070–1, TUZ399098), 29 June 2025, Prous leg. • 1♀ (OLC), 29 June 2025, Lønnve leg. • 1♀ (SDEI), 29 June 2025, Liston leg.

Habitus and variability (Figs 4, 5). Length 4.0–5.5 mm. Femora from mostly black to mostly pale; upper head usually completely black, but orbits occasionally brownish; upper rear edge of pronotum sometimes with small pale area. Two specimens from Nuuk (DEI-GISHym40557, DEI-GISHym40558) are smaller (Fig. 5), have a somewhat smaller subapical tooth of the claw than most other specimens, and the mesonotum and mesepisternum are shinier.

Habitats. Favours moist areas, such as snow-patch edges and the banks of streams, and is absent or very scarce in drier places, even when the larval host plant is present.

Host plants and biology. The only known host is *Bistorta vivipara* (L.) Delarbre (Prous et al. 2025). Based on some of the larvae found in the field, females might typically lay two eggs per leaf (Fig. 6). No male specimens are known.

Figure 4. *Euura excisa* female (TUZ399053), body length ca. 5.0 mm. Photos: M. Prous.

Distribution. Definite records are only from Arctic Europe and Greenland (Smith 1979): principally in tundra but also from open areas in boreal forest regions of Fennoscandia (around 66°N, e.g. Kuusamo Region in Finland and Västerbotten Province in Sweden). The host plant is widespread and abundant in Iceland, but *E. excisa* has not so far been recorded there.

Genetics. The COI sequencing of four specimens yielded five different variants (Fig. 7). The dominant variants of the two atypical specimens from Nuuk (DEI-GISHym40557, 40558) are identical to a specimen from Sweden (SL69_G1) and 0.4% different from the typical specimens from Kapisillit and Narsarsuaq. A larva from Kapisillit (TUZ399073) has a unique sequence that is almost identical (0.2% different) to a female from Narsarsuaq (TUZ399053). Curiously, the dominant variant of the Narsarsuaq (TUZ399053) specimen is identical (1078 bp of COI) to *Euura declinata* from Estonia (Fig. 7). Two of the specimens (DEI-GISHym40558, TUZ399053) also yielded additional variants of COI (one each) that are very similar to the other *E. excisa* sequences (0.2–0.4% different).

Comparing nuclear genes (Fig. 8), the atypical specimens from Nuuk (DEI-GISHym40557, DEI-GISHym40558) are identical and 0.00–0.08% different from three Fennoscandian *E. excisa* (Finland and Sweden, with at least 3425 bp available). The sequenced specimens from Kapisillit and Narsarsuaq (TUZ399073, TUZ399053) are identical and 0.11–0.43% different from all the other specimens (Nuuk and Fennoscandia). The atypical specimens from Nuuk are much more heterozygous (possess distinct haplotypes for five nuclear genes out of seven) compared to the specimens from Kapisillit (two nuclear genes out of seven with two haplotypes) and Narsarsuaq (all five sequenced nuclear genes homozygous). The haplotypes of the Nuuk specimens are very similar to the haplotypes of Fennoscandian specimens, hence the higher similarity between them in distance calculations compared to the specimens from Kapisillit and Narsarsuaq.

Figure 5. *Euura excisa* female (DEI-GISHym40558), body length ca. 4.0 mm. Photo: Stefan Olberg.

Figure 6. *Euura excisa* larvae on *Bistorta vivipara*. Early (left) and late instar larvae, respectively from Kapisillit and Narsarsuaq, both photographed on 28 June 2025. Photos: M. Prous.

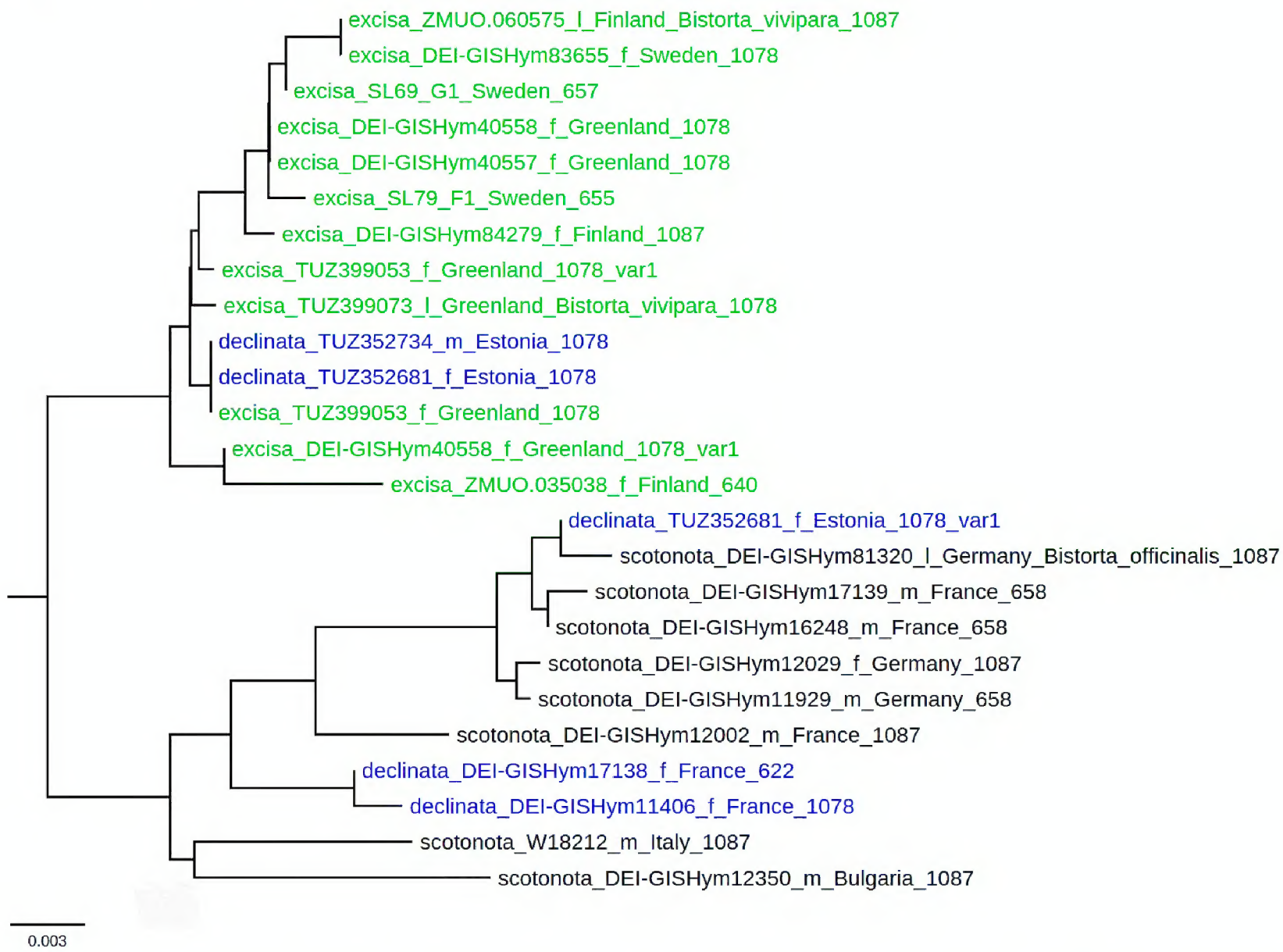

Figure 7. Distance tree of *Euura excisa* and its closest relatives *E. declinata* and *E. scotonota* (see Prous et al. 2025), based on COI (sequence length given after the country name). "var" at the end of some sequence labels means that these sequences are secondary intraindividual COI variants. m – male, f – female, l – larva.

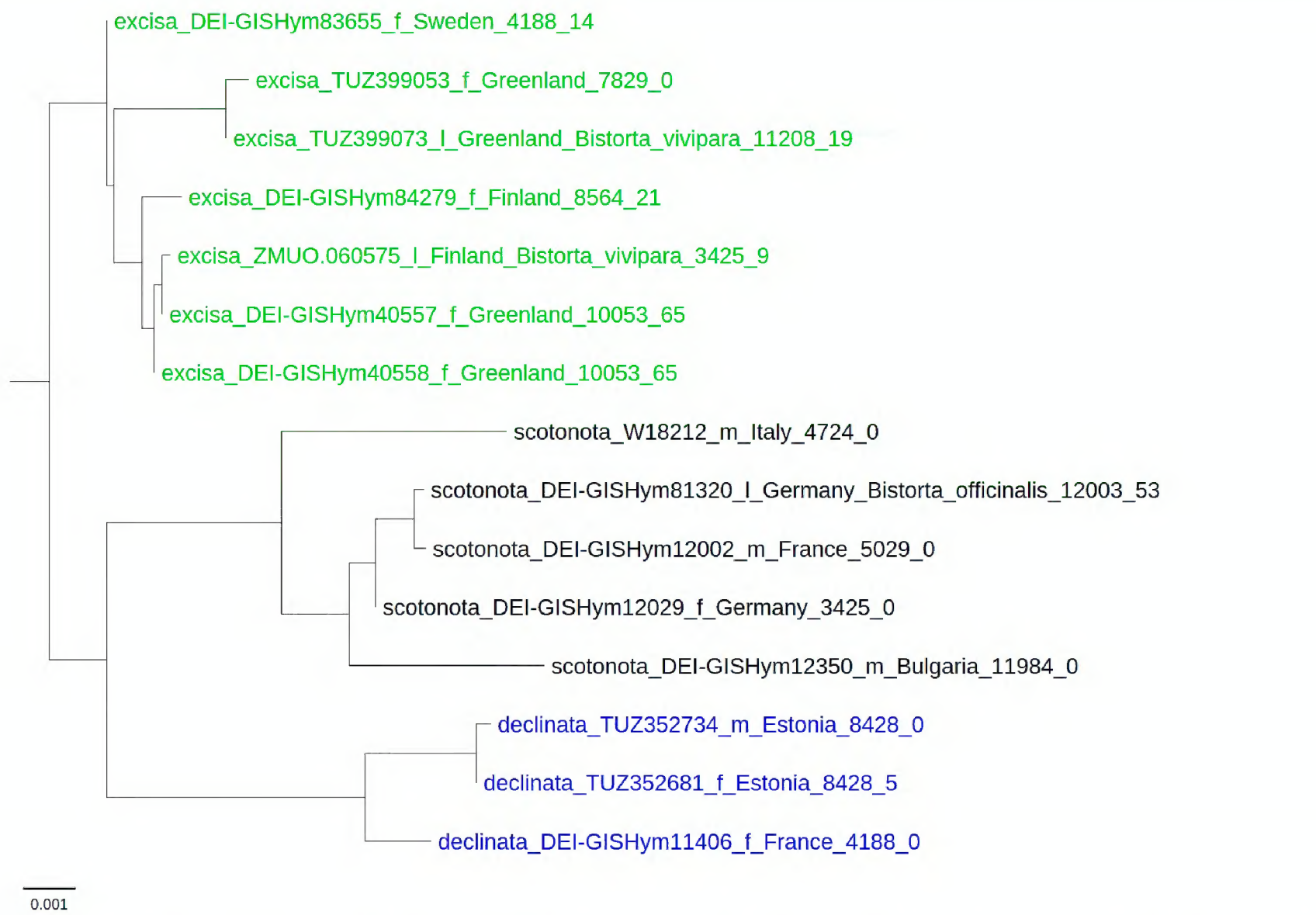

Figure 8. Distance tree of *Euura excisa* and its closest relatives *E. declinata* and *E. scotonota* (see Prous et al. 2025), based on nuclear genes (sequence length and number of heterozygous positions given after the country name). m – male, f – female, l – larva.

Euura obducta (Hartig, 1837)

Material examined. Greenland. Narsarsuaq • 1♀ (SDEI; DEI-GISHym81440), 15 June 2025, Liston leg. • 1♀ (SDEI), 16 June 2025, Liston leg. • 1 larva *ex ovo* (TUZ; TUZ399076), 18 June 2025, Prous leg. • 3♀♀ (OLC), 18 June 2025, Lønnve leg. • 1♀ (OLC), 20 June 2025, Lønnve leg. • 1♀ (TUZ; TUZ109630), 22 June 2025, Lønnve leg. • 1♀ (SDEI), 22 June 2025, Liston leg. Qassiarsuk • 3♀♀ (SDEI), 21 June 2025, Liston leg. • 1♀ (TUZ; TUZ399055), 21 June 2025, Prous leg. • 2♀♀ (OLC), 21 June 2025, Lønnve leg. Nuuk • 1♀ (OLC), 26 June 2025, Lønnve leg. • 8♀♀ (OLC), 3 July 2025, Lønnve leg. • 4♀♀ (SDEI), 3 July 2025, Liston leg. Kapisillit • 1♀ (OLC), 27 June 2025, Lønnve leg. • 2♀♀ (OLC), 28 June 2025, Lønnve leg. • 1♀ (OLC), 29 June 2025, Lønnve leg. • 1♀ (OLC), 30 June 2025, Lønnve leg. • 1♀ (TUZ; TUZ109631), 27 June 2025, Lønnve leg. • 2♀ (TUZ; TUZ109632, TUZ399093), 2 July 2025, Prous leg. • 1♀ (SDEI), 28 June 2025, Liston leg. 1♀ (SDEI; DEI-GISHym81284), 28 June 2025, Liston leg. • 4♀♀ (SDEI), 30 June 2025, Liston leg.

Habitus and variability (Fig. 9). Length 4.5–5.5 mm. Metafemur nearly entirely black and forewing stigma mainly blackish (clearly darker than costa) in all specimens, except for DEI-GISHym81284 with metafemur ventral surface nearly entirely pale, dorsal surface only darkened at tip, and forewing stigma largely pale (little darker than costa).

Habitats. Specimens were collected mostly from patches of grass containing *Calamagrostis canadensis* (Michx.) P.Beauvois. A female was offered *C. canadensis* and *Poa nemoralis* L. for oviposition but laid eggs only on the latter (a reared larva: Fig. 9).

Host plants and biology. Various genera of Poaceae, such as *Poa* L., *Elymus* L., *Phleum* L., and *Dactylis* L., are reliably recorded hosts (Prous et al. 2025). *Carex* L. is often also listed, but this seems to be based on a single observation by Conde (1934) and would benefit from verification. Males are extremely rare and known only from central Europe. At least two annual broods are possible, under favourable conditions.

Distribution. Occurs widely in the Holarctic (Sundukov 2017; Goulet and Bennett 2021; Smith 1979) and in Europe from Portugal northwards into the Arctic areas of Fennoscandia (own observations). Also recorded in Iceland (Ólafsson 1991).

Remarks. One specimen was collected from an inflorescence of *Taraxacum* sp. (OL).

Genetics. Two sequenced specimens (TUZ399055, TUZ399093) both yielded multiple apparently functional COI variants. The dominant variant (in terms of sequencing output) from TUZ399055 is identical to a specimen from northern Sweden (specimen SL81_C8 in BOLD), and the same variant is also found in TUZ399093 as the second most common variant. The dominant variant from TUZ399093 is a minimum of 1.8% different from the other *E. obducta* sequences (the closest cluster contains

Figure 9. *Euura obducta* female (TUZ399055), body length ca. 5.0 mm (top), and larva (TUZ399076), length 11 mm (bottom). Photos: M. Prous.

specimens from Canada, Europe, and Iceland). The dominant variant of TUZ399093 is 3.1% (1078 bp) or 3.6% (including only 658 bp of the barcoding region) different from the dominant variant of TUZ399055. The second most common variant from TUZ399055 is closest to some specimens from Finland and the United Kingdom (minimum of 0.8% different), which together form the most divergent COI cluster in *E. obducta*. This divergent *E. obducta* COI cluster is 3.1–5.2% different from the others. The additional less common variants from TUZ399055 (one) and TUZ399093 (two) are unique sequences diverging by a minimum of 0.6–0.9% from the others in BOLD.

Based on nuclear genes, two specimens from Greenland are identical but differ by 0.1%–0.3% from three other specimens (two from Finland, one from Germany), depending on the selection of nuclear genes (the three European specimens are identical to each other but based on differing available selections of nuclear genes).

Euura obscuripes (Holmgren, 1883)

Nematus obscuripes Holmgren, 1883: 144–145, pl. 1 fig. 5. Lectotype ♀ (NHRS-HEVA000006456; designated by Prous et al. 2025), Russia, Novaya Zemlya, Matochkin Strait (73.3°N, 55.6°E), 1875, NHRS.

Nematus borealis Marlatt, 1892: 133. Holotype ♂ (Fig. 10), Greenland, Disko Island (69.75, -53.5), 27.06.1891–02.07.1891 (dates based on Peary and Peary 1893: 12–16), Mengel and Hughes leg., ANSP. Syn. nov.

Amauronematus groenlandicus Malaise, 1933: 3–4. Holotype ♀ (Fig. 11), Greenland, Wollaston Forland, Landingsdalen (74.47, –19.13), 28.07.1929, Knaben leg., ZMUN. Syn. nov.

Material examined. One of the primary type specimens listed above (*Nematus borealis*) was not examined directly, but photos of it were sent by Jason Weintraub (ANSP). Additional record: Zackenberg Research Station (74.467, –20.567) • 1♀ (SYKE; grhym-00071), 30.07.2009, Roslin leg.

The identity of the holotype of *Amauronematus groenlandicus* Malaise was discussed by Prous et al. (2025), who considered it to be possibly conspecific with *E. obscuripes*. A closer examination of the single barcoded specimen from Greenland (grhym-00071 in BOLD; Fig. 11) revealed that it matches well with the holotype of *A. groenlandicus* (the barcoded specimen is somewhat darker). Both were collected on the Wollaston Forland Peninsula (North-East Greenland). The barcoded specimen belongs to the cluster BOLD:AAQ0427, which contains at least *Euura obscuripes* (specimen DEI-GISHym31073; see Prous et al. 2025: 180), but possibly also some other species of the *Euura toeniata* species group. The colouration of the *A. groenlandicus* holotype and specimen grhym-00071 is similar to paler females from Europe (formerly known as *Amauronematus poppii* Konow, 1904), but the barcode sequence of grhym-00071 is closest to a specimen from California (DEI-GISHym31073), which in its darker colouration and nuclear genes is a more typical form of *E. obscuripes* (see Prous et al. 2025). *Nematus borealis* Marlatt is here synonymised with *E. obscuripes* (external morphology is consistent with this), but this requires confirmation by studying genitalia and genetics. The genitalia of the *Nematus borealis* holotype have been extracted but are unfortunately now lost (the associated microvial is empty, J. Weintraub, personal communication).

Genetics. A barcoded specimen from Northeast Greenland (Zackenberg Research Station; grhym-00071 in BOLD) is closest to unidentified *Euura toeniata* group specimens from northern Canada (0.3% different).

Euura punctifrons (Malaise, 1921)

Notes. External morphology (black; labrum, tibiae, femora apically, clypeus and tegula partly pale or brown; claws with minute subapical tooth) and the saw of a specimen in NHMD (zmuc00023366, from nSW Greenland, 65.45, –52.217; also in BOLD, but without sequence data) fit well with *Euura punctifrons*, except that the saw (Fig. 12) has 14 serrulae compared to 16–17 in Fennoscandian specimens. The saw of *E. excisa* is similar, but serrulae are somewhat more protruding and the gaps between serrulae larger than in *E. punctifrons* (Fig. 12). Benson (1962) mentioned *Pachynematus parvilabris* (Thomson, 1863) from Greenland (Nugssuaq, 70.69, –54.57), which was not found in NHMD but is probably the same species as zmuc00023366.

Figure 10. *Euura obscuripes* male. Holotype of *Nematus borealis* Marlatt, 1892 (ANSP). Scale bar: 2 mm.

Figure 11. *Euura obscuripes* females. Holotype of *Amauronematus groenlandicus* Malaise, 1933, body length ca. 7.5 mm (top; photo: M. Prous), and a barcoded specimen grhym-00071, body length ca. 7.5 mm (bottom; photo: Marko Mutanen).

Figure 12. Saws of *Euura punctifrons* zmuc00023366 (top) and *E. excisa* TUZ109712. Photos: M. Prous.

Euura vaga (Fabricius, 1781)

Material examined. Greenland. Kapisillit • 1♀ (TUZ; TUZ399065), 28 June 2025, Prous leg. • 1 larva (TUZ; TUZ399074), 28 June 2025, Olsen leg. • 1♀ (TUZ; TUZ399069), 29 June 2025, Prous leg. • 1♀ (SDEI), 2 July 2025, Liston leg.

Habitus and variability (Fig. 13). Length 6.0–6.5 mm. No significant variability.

Habitat. Two adults were from wet depressions dominated by *Carex* and *Eriophorum* L., in a marsh/heath complex. A third adult was collected from a wet habitat at higher altitude (300–400 m). The larva (Fig. 13) was swept beside a river, in a spot dominated by Poaceae and one or more *Salix* species.

Host plants and biology. Only *Carex* spp. have been recorded as hosts (e.g. by Benander 1966; Kangas 1985). At least two annual broods are possible, under favourable conditions. Males are extremely rare in Europe, but apparently frequent in parts of North America.

Distribution. Occurs widely in the Holarctic (Sundukov 2017; Goulet and Bennett 2021; Smith 1979). Also recorded in Iceland (Ólafsson 1991).

Remarks. Not previously recorded in Greenland.

Genetics. The COI of the sequenced larva (TUZ399074) is closest to specimens from Canada and several European countries (minimum difference 0.5%). Based on the haplotypes of most nuclear genes (six), the Greenlandic specimen falls well within the variation present in European specimens (distances to closest haplotypes 0.0–0.4%), except that TRRAP is the most divergent among the sequenced *E. vaga* (1.1–1.2% different), while the distances between the other seven specimens for that nuclear gene are 0.0–1.0%.

Pristiphora laricis (Hartig, 1837)

Material examined. Greenland • Narsarsuaq, 101♀♀, 51♂♂ (OLC, SDEI, TUZ; including TUZ399047–8, TUZ109636–9, TUZ109640, TUZ109641–54, TUZ399054, TUZ109655–7, TUZ109633–5, TUZ399060–2, TUZ109658), 13–25 June 2025.

Habitus and variability (Fig. 14). Length; female (4.0) 4.5–5.5 mm, male 4.0–5.0 mm. Female: metafemur from nearly completely black to completely pale. Abdominal tergum 10 from black to pale.

Figure 13. *Euura vaga*. Female TUZ399065, body length ca. 6.0 mm (top), and larva TUZ399074, length 15 mm. Photos: M. Prous.

Figure 14. *Pristiphora laricis*. Female (TUZ109648), body length ca. 5.5 mm, and male (TUZ109656), body length ca. 4.5 mm. Photos: M. Prous.

Habitat. Specimens were found throughout the area designated as the Arboretum Groenlandicum, an area covering about 150 ha to the east and north of Narsarsuaq settlement.

Host plants and biology. Larvae feed on several *Larix* species (Prous et al. 2017). Established in the Greenlandic Arboretum are at least *Larix decidua* Mill., *L. sibirica* Ledeb., *L. laricina* (Du Roi) K.Koch, and *L. gmelinii* (Rupr.) Göpp., of which *L. sibirica* was the first non-native tree species planted there, in 1966, and is now the most numerous larch species (Meilby et al. not dated). In Europe, *P. laricis* is regularly bivoltine but can be univoltine at high altitudes in the Alps (Pschorn-Walcher and Altenhofer 2000).

Distribution. Previously only known from the Palaearctic, where it occurs practically throughout the natural range of *Larix*, from the mountains of central Europe eastwards through northern Russia and into Korea, northern China, and Japan (Sundukov 2017). It is also widespread nearly everywhere where larches have been planted in Europe outside their natural ranges.

Remarks. *Pristiphora laricis* was very abundant at Narsarsuaq, and many individuals were swept from plants other than *Larix*. It would have been possible, with little effort, to collect a much larger number of specimens. One female (TUZ109658) was collected by sweeping the ground with *Salix herbacea*, about 2 km from the nearest *Larix* tree. The first Greenlandic

specimens of *P. laricis* were collected at Narsarsuaq in late July 2018 by S. Harding. The occurrence of the species in Greenland was already indicated by Taeger et al. (2018).

Genetics. The COI of two sequenced specimens (TUZ399047, TUZ399048) is identical to a few specimens from Finland and Germany. Based on nuclear genes, the Greenlandic specimens are 0.2% different from each other and are closest to a specimen from Finland (minimum distance 0.04%). The other specimens with available nuclear data (two from Estonia, one from Norway) are 0.4–0.5% different from the Greenlandic specimens.

Table 1. List of Greenland sawflies and their distribution.

Species	N	NW	NE	nSW	sSW	SE	S
Ametastegia pallipes							×
Euura amentorum	?×		×		×		
Euura cornuta		×	×			×	
Euura excisa		×			×	×	×
Euura obducta					×	×	×
Euura obscuripes			×	×		×	
Euura punctifrons		?×		×			
Euura vaga					×		
Pristiphora laricis							×

Based on Benson (1962), Vilhelmsen (2015), and original data. Subdivision of Greenland into zoogeographic regions after Böcher et al. (2015: p. 22, fig. 1 [map]).

Discussion

Accidental importation and establishment of insect species in territories outside their natural range have increased worldwide in recent decades, and the diverse and sometimes far-reaching ecological and economic impacts have been widely documented and discussed (e.g. Kenis et al. 2009; Reaser et al. 2007). In the context of biogeographical studies, such introductions can obscure the natural composition of a fauna, a problem that is obviously more severe in regions where the native fauna has not been well studied. The faunas of the archipelagos of the northern North Atlantic belong at least partly in this category. While our knowledge of the native insect fauna, particularly sawflies, of Svalbard, Shetland, the Faroes, and Greenland can probably be regarded as relatively complete, it is suspected that this may not be the case for Iceland. Unfortunately, as discussed below, a comparison with the Icelandic fauna seems to be necessary if the origins of the Greenlandic sawfly fauna are to be more fully understood.

Of the six species of sawfly recorded in south and south-west Greenland in 2025, *Pristiphora laricis* has obviously been introduced by humans, because it is monophagous on a plant genus that itself has only rather recently (since around 1930) been deliberately introduced to Greenland (Meilby et al. 2019). However, the status of some of the other species as native or introduced to Greenland is equivocal. The Norse colonists of Greenland in the 9th century AD brought livestock from Iceland with them, including cattle, sheep, and goats. To sustain the animals on the voyage, they would certainly have brought with them a quantity of fodder, presumably fresh hay. In fair weather, the voyage from western Iceland to Greenland's Eastern Settlement, which included the area around Narsarsuaq, took little more than a week. One can easily imagine immature stages of the grass-feeding *Euura obducta* having been transported in this way and surviving the voyage. Indeed, Fredskild (1978) concluded from palaeobotanical evidence that *Poa annua*, a potential host of *E. obducta*, was "beyond doubt immediately introduced" during the initial Norse colonisation (ca. 895 AD) of the Greenlandic Eastern Settlement. Successful subsequent establishment of *E. obducta* would have been made considerably easier, compared to a sexually reproducing species, by its normally parthenogenetic reproduction. Notably, the latter trait is shared by all four *Euura* species that occur in southern Greenland, as well as *Ametastegia pallipes*. Therefore, it seems possible that any of these species might at some time have been introduced from elsewhere, although the host plant associations and biology of *Euura amentorum* and *E. excisa* make this scenario seem less likely for them. In the case of *Ametastegia pallipes*, an accidental introduction would have been greatly facilitated by the habit of mature larvae of *Ametastegia* of boring into various organic substrates (e.g. dead wood, pithy stems), where they complete their development to adults. It should also be borne in mind that the sawfly fauna of Iceland, an island no less remote than Greenland from potential sources of natural colonisation, may itself include a significant number of species that were brought there by humans in early historical times.

Although there are far fewer comparable genetic data from North America (particularly an almost complete lack of nuclear gene sequences), six of the Greenlandic species (*Ametastegia pallipes*, *Euura amentorum*, *E. excisa*, *E. obducta*, *E. vaga*, *Pristiphora laricis*) appear more likely to be of European origin based on genetics. *Pristiphora laricis* and *Euura excisa* are not even known from North America, although *E. excisa* could potentially be present. The high genetic similarities between the specimens from Greenland and Europe are consistent with introductions that occurred during the last ca. 1100 years (as already mentioned, *P. laricis* must have been introduced relatively recently, since the first *Larix* were planted in Greenland only within the last approximately 100 years), but much more genetic data would be needed to estimate the time scale more reliably. As pointed out by Gårdman et al. (2026), goods imported to Greenland are currently overwhelmingly from Denmark, continuing the traditionally very strong trade links between Greenland and northern Europe. Two of the Greenlandic species (*Euura cornuta*, *E. obscuripes*) probably originate from North America, based on COI data, perhaps having dispersed through Ellesmere Is-

land (a larva BIOUG16667-C02 from there in BOLD is possibly *E. cornuta*). They may even be the only native sawfly species in Greenland, although no genetic data are available for *Euura punctifrons*.

The zoogeography of the Greenlandic insect fauna, as discussed by Böcher et al. (2015: 23), exhibits some paradoxical patterns, for which convincing explanations are currently largely lacking. While the faunal affinity of Greenlandic species assemblages of several groups of terrestrial arthropods has been judged to be strongly Nearctic (e.g. spiders, butterflies, caddisflies, and muscid flies), other groups are dominated by Palaearctic and Holarctic species (e.g. beetles and springtails), with a complete absence of purely Nearctic elements among the beetles (Böcher et al. 2015). Böcher et al. (2015) concluded that the higher taxa that are dominated by Nearctic elements tend to be those that are more easily dispersed, whether passively or actively, and that the more earthbound organisms are markedly Palaearctic. In the present authors' opinion, sawflies belong more to the latter category, with the qualification that while there is ample evidence of frequent and large-scale dispersal within landmasses (e.g. Liston et al. 2020), there is practically no evidence for naturally occurring dispersal over larger waterbodies. Our hypothesis regarding the long-standing importance of human activities in shaping the composition of the Greenlandic sawfly fauna introduces a new factor to this complicated picture.

The interesting case of identical COI sequences shared by *Euura declinata* (host *Bistorta officinalis* Delarbre) from Estonia and some *Euura excisa* from Greenland (Fig. 7) could be explained by mitochondrial introgression or incomplete lineage sorting (retention of ancestral polymorphism after speciation). However, nuclear genes clearly support *E. declinata* and *E. excisa* as separate species (Fig. 8), indicating that incomplete lineage sorting (which would be more likely evident in nuclear genes due to their slower mutation rate and larger effective population size compared to mitochondrial DNA) is a less likely explanation compared to mitochondrial introgression (Linnen and Farrell 2007; Prous et al. 2020). *Euura excisa* is not known in Estonia, but might once have been present there, or more abundant than now, because its host *Bistorta vivipara* was historically more common (https://ottluuk.github.io/atlas/taxon/Bistorta_vivipara.html). *Euura excisa* and *E. declinata* could be sympatric also elsewhere, e.g. in some places in the Republic of Karelia (Russia) where both *Bistorta* species occur (Kravchenko et al. 2015). Hybridisation between *E. excisa* females (males not known) and *E. declinata* males, and subsequent backcrossing of the hybrid females with *E. declinata* males, could have introduced the mitochondrion of *E. excisa* to *E. declinata* without detectable nuclear gene flow even after a small number (~10) of generations.

The sawfly species currently established in Greenland probably play no important role as pollinators. As also observed in other parts of their range, they are species that rarely, if ever, visit flowers. *Euura amentorum* is an exception, because its females visit female willow catkins to oviposit, and outside Greenland, they have been seen to feed at male catkins. However, any benefit to the host through pollination by *E. amentorum* is surely negated by the destruction of female reproductive organs and seeds by its larvae.

The potential for successful establishment of further sawfly species in Greenland is huge. Many native Greenlandic plant taxa are known to be hosts of sawfly larvae in northern Fennoscandia, where climatic conditions are quite similar (at least to coastal areas of southern Greenland). Just one example is *Betula pubescens* Ehrh., on which at least 40 sawfly species feed in Lapland, but none in Greenland (based on a thorough review of the literature and extensive unpublished original data obtained by M. Mutanen, V. Vikberg, and others).

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